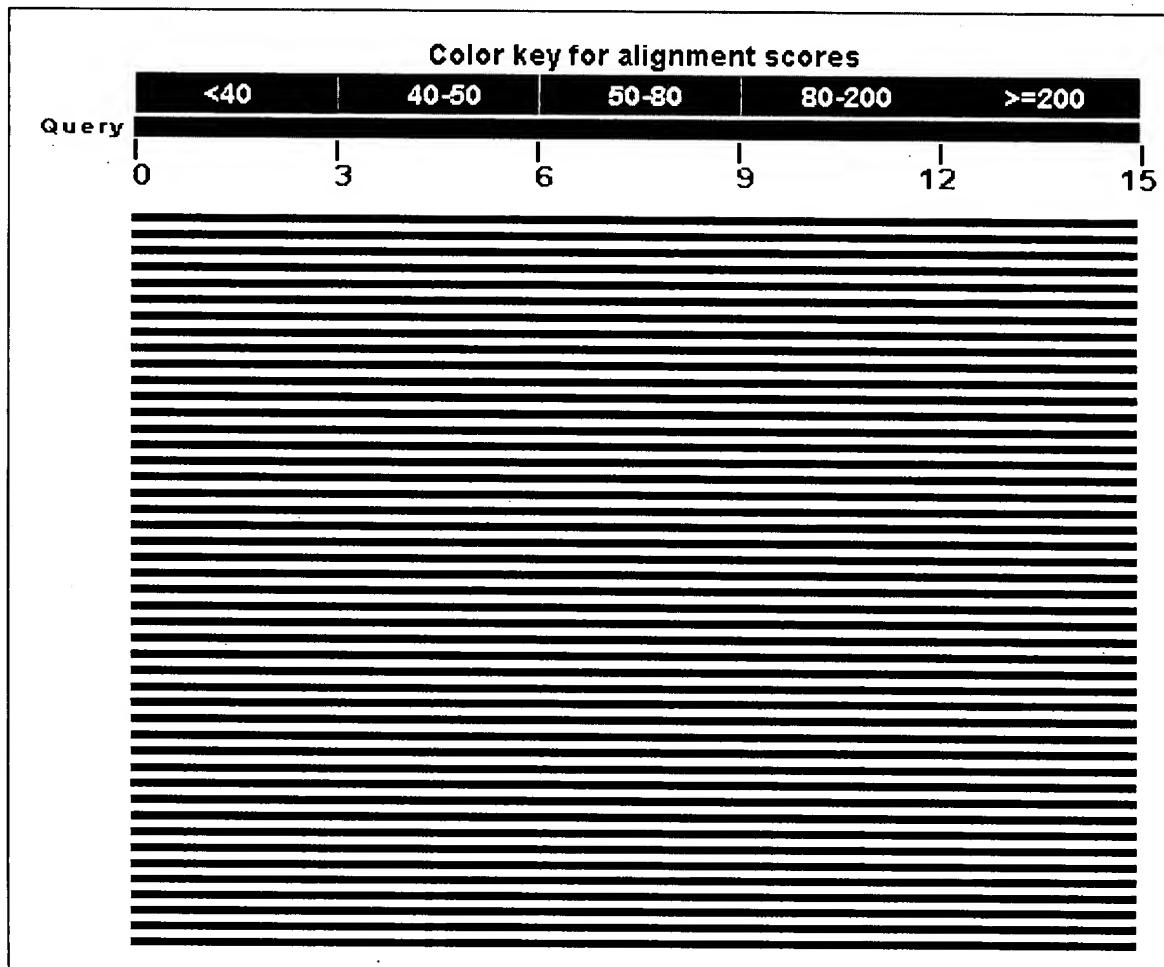


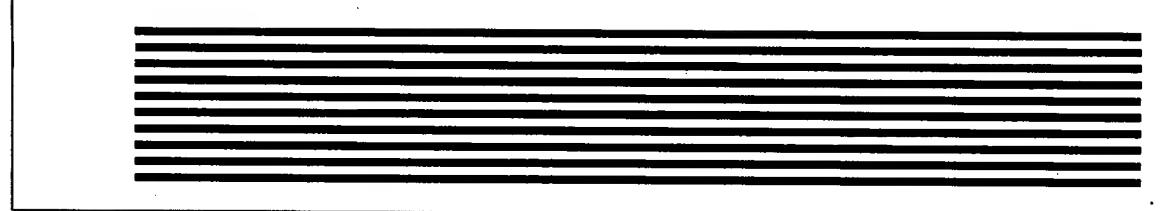
BLAST Basic Local Alignment Search Tool**Job Title:** Nucleotide sequence (15 letters)

- Your search parameters were adjusted to search for a short input sequence.
-
-

BLASTN 2.2.17 (Jun-24-2007)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 8HV76DVM014 **Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 5,454,516 sequences; 20,739,661,006 total letters

Query= Length=15**Distribution of 74 Blast Hits on the Query Sequence**



[REDACTED]

Distance tree of results NEW

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **R**

Sequences producing significant alignments:

(Click headers to sort columns)

AM468046.2 Vitis vinifera contig VV78X022861.5, 30.2 30.2 100% 33 100%
whole genome shotgun sequence

AC202214.3 Pea Aphid NOVECTOR VMRC38-20-A9 () 30.2 30.2 100% 33 100%
complete sequence

NM_018666.2 Homo sapiens sarcoma antigen 1 30.2 30.2 100% 33 100% **UG**
(SAGE1), mRNA

CP000660.1 Pyrobaculum arsenaticum DSM 13514, 30.2 30.2 100% 33 100%
complete genome

AC188814.3 Gallus gallus BAC clone CH261-93D11 30.2 30.2 100% 33 100%
from chromosome z, complete sequence

XM_770878.1 Cryptococcus neoformans var. 30.2 30.2 100% 33 100% **G**
neoformans B-3501A hypothetical
protein (CNBD3780) mRNA, complete cds

AC189953.7 Rhesus Macaque BAC CH250-253F13 () 30.2 30.2 100% 33 100%
complete sequence

CP000569.1 Actinobacillus pleuropneumoniae L20 30.2 30.2 100% 33 100%
serotype 5b complete genome

XM_001309841.1 Trichomonas vaginalis G3 surface 30.2 30.2 100% 33 100% **G**
antigen BspA-like (TVAG_272400) mRNA,
complete cds

XM_001309840.1 Trichomonas vaginalis G3 surface 30.2 30.2 100% 33 100% **G**
antigen BspA-like (TVAG_272390) mRNA,
complete cds

XM_001304479.1 Trichomonas vaginalis G3 surface 30.2 30.2 100% 33 100% **G**
antigen BspA-like (TVAG_422450) mRNA,
complete cds

AC193609.2 Gallus gallus BAC clone TAM33-18K5 30.2 30.2 100% 33 100%
from chromosome z, complete sequence

AE016815.3 Ashbya gossypii (= Eremothecium 30.2 30.2 100% 33 100%
gossypii) ATCC 10895 chromosome II,
complete sequence

XM_417055.2 PREDICTED: Gallus gallus similar to 30.2 30.2 100% 33 100% **UG**
Chromosome condensation 1-like
(LOC418861), mRNA

CT573001.7 Zebrafish DNA sequence from clone 30.2 30.2 100% 33 100%
CH211-180A12 in linkage group 12,
complete sequence

XM_527015.2 PREDICTED: Pan troglodytes cation 30.2 30.2 100% 33 100% **G**
channel, sperm associated 3
(CATSPER3), mRNA

BC110384.1 Homo sapiens cation channel, sperm 30.2 30.2 100% 33 100% **UG**
associated 3, mRNA (cDNA clone
MGC:117279 IMAGE:5166215), complete
cds

BN000272.1 TPA: TPA_exp: Homo sapiens mRNA for 30.2 30.2 100% 33 100% **G**
CatSper3

CT737238.2 Pan troglodytes chromosome X clone 30.2 30.2 100% 33 100%

CH251-56J08 map Xq28, complete
sequence

AC188312.1	Taeniopygia guttata chromosome UNK clone TGMCBa-32H12, complete sequence	30.2	30.2	100%	33	100%	
XR_012260.1	PREDICTED: Macaca mulatta similar to titin isoform N2-A (LOC703527), mRNA	30.2	30.2	100%	33	100%	UG
AC139131.19	Mus musculus chromosome 7, clone RP23-301N20, complete sequence	30.2	30.2	100%	33	100%	
BC101692.1	Homo sapiens cation channel, sperm associated 3, mRNA (cDNA clone MGC:126741 IMAGE:8069198), complete cds	30.2	30.2	100%	33	100%	UG
AC163351.2	Mus musculus BAC clone RP23-150D4 from chromosome 13, complete sequence	30.2	30.2	100%	33	100%	
NM_178019.1	Homo sapiens cation channel, sperm associated 3 (CATSPER3), mRNA	30.2	30.2	100%	33	100%	UE G
AE017344.1	Cryptococcus neoformans var. neoformans JEC21 chromosome 4, complete sequence	30.2	30.2	100%	33	100%	
AC004764.1	Homo sapiens chromosome 5, P1 clone 255g5 (LBNL H61), complete sequence	30.2	30.2	100%	33	100%	
AC158619.12	Mus musculus 10 BAC RP23-291O3 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	30.2	30.2	100%	33	100%	
XM_538633.2	PREDICTED: Canis familiaris similar to cation channel, sperm associated 3 (LOC481512), mRNA	30.2	30.2	100%	33	100%	UG
AC122483.5	Mus musculus BAC clone RP24-366B4 from chromosome 6, complete sequence	30.2	30.2	100%	33	100%	
AC123801.4	Mus musculus BAC clone RP24-374A1 from chromosome 15, complete sequence	30.2	30.2	100%	33	100%	
AC122402.2	Mus musculus BAC clone RP24-108B4 from chromosome 13, complete sequence	30.2	30.2	100%	33	100%	
AC122900.3	Mus musculus BAC clone RP23-39N24 from 15, complete sequence	30.2	30.2	100%	33	100%	
AC164104.5	Mus musculus BAC clone RP23-428G7 from chromosome 6, complete sequence	30.2	30.2	100%	33	100%	
XM_384727.1	Gibberella zeae PH-1 chromosome 2 hypothetical protein (FG04551.1) partial mRNA	30.2	30.2	100%	33	100%	G
AC163759.4	Pan troglodytes BAC clone CH251- 258I24 from chromosome unknown, complete sequence	30.2	30.2	100%	33	100%	
AC079851.14	Homo sapiens 12 BAC RP11-349L8 (Roswell Park Cancer Institute Human BAC Library) complete sequence	30.2	30.2	100%	33	100%	
AC011592.5	Homo sapiens chromosome 3, clone RP11-42F12, complete sequence	30.2	30.2	100%	33	100%	E
XM_570454.1	Cryptococcus neoformans var. neoformans JEC21 hypothetical protein (CND02560) partial mRNA	30.2	30.2	100%	33	100%	UG
AC012176.8	Homo sapiens chromosome 16 clone RP11-206F18, complete sequence	30.2	30.2	100%	33	100%	
CR956411.6	Pig DNA sequence from clone CH242-	30.2	30.2	100%	33	100%	

282N1 on chromosome 17, complete
sequence

AC096642.2	Homo sapiens chromosome 1 clone RP11- 30.2 30.2 100% 33 100%
AP008208.1	Oryza sativa (japonica cultivar- 30.2 60.5 100% 33 100%
BX908755.10	group) genomic DNA, chromosome 2 30.2 30.2 100% 33 100%
AL355499.15	Zebrafish DNA sequence from clone 30.2 30.2 100% 33 100%
BKEY-67F11 in linkage group 3, complete sequence	
AC159477.9	Human DNA sequence from clone RP11- 30.2 30.2 100% 33 100%
328K6 on chromosome 6, complete sequence	
AC023655.1	Mus musculus 10 BAC RP23-95I8 30.2 30.2 100% 33 100%
(Roswell Park Cancer Institute	
(C57BL/6J Female) Mouse BAC Library)	
AC023356.8	complete sequence
AL023655.1	Human DNA sequence from clone RP1- 30.2 30.2 100% 33 100%
242N11 on chromosome 6p22.3-23, complete sequence	
AC090516.3	Homo sapiens chromosome 15 clone 30.2 30.2 100% 33 100%
RP11-319G10 map 15q15, complete sequence	
BX548034.14	Zebrafish DNA sequence from clone 30.2 30.2 100% 33 100%
DKEY-106M16 in linkage group 1, complete sequence	
AL713962.14	Mouse DNA sequence from clone RP23- 30.2 30.2 100% 33 100%
3D5 on chromosome 11, complete sequence	
CR925766.2	Zebrafish DNA sequence from clone 30.2 30.2 100% 33 100%
DKEYP-12B2 in linkage group 18, complete sequence	
BX950182.13	Zebrafish DNA sequence from clone 30.2 30.2 100% 33 100%
CH211-203B8 in linkage group 18, complete sequence	
AF432876.1	Homo sapiens putative one-repeat 30.2 30.2 100% 33 100%
calcium channel mRNA , complete cds	UE G
AC090839.1	Caenorhabditis briggsae cosmid 30.2 30.2 100% 33 100%
CB022018 , complete sequence	
AC117984.2	Homo sapiens chromosome 16 clone CTD- 30.2 30.2 100% 33 100%
2503H21 , complete sequence	
BX511256.9	Zebrafish DNA sequence from clone 30.2 30.2 100% 33 100%
DKEY-58M10 in linkage group 1, complete sequence	
AC008670.6	Homo sapiens chromosome 5 clone CTB- 30.2 30.2 100% 33 100%
3601 , complete sequence	
AP003977.3	Oryza sativa (japonica cultivar- 30.2 60.5 100% 33 100%
group) genomic DNA, chromosome 2, BAC	
clone:OJ1006_A02	
AP003974.3	Oryza sativa (japonica cultivar- 30.2 30.2 100% 33 100%
group) genomic DNA, chromosome 2, BAC	
clone:OJ1003_F05	
AF274856.3	Homo sapiens chromosome X clone RP11- 30.2 30.2 100% 33 100%
1007I13 map q28, complete sequence	

AF274855.3	Homo sapiens chromosome X clone RP11-366F6 map q28, complete sequence	30.2	30.2	100%	33	100%
U82696.2	Homo sapiens chromosome X clone ICRFXc104-F064, ICRFXc104-G0799, Qc-14E2, Qc-13D8, Qc-7G11, ICRFXc104-E0681, Qc-11C8, Qc-9A9 map q28, complete sequence	30.2	30.2	100%	33	100%
AC160944.2	Pan troglodytes BAC clone CH251-7D22 from chromosome unknown, complete sequence	30.2	30.2	100%	33	100%
BX294104.7	Zebrafish DNA sequence from clone CH211-245I22 in linkage group 1, complete sequence	30.2	30.2	100%	33	100%
NM_208333.1	Ashbya gossypii ATCC 10895 ABR034Wp (AGOS_ABR034W) mRNA, complete cds	30.2	30.2	100%	33	100% G
AJ278111.1	Homo sapiens mRNA for putative tumor antigen (SAGE gene)	30.2	30.2	100%	33	100% UE
AP002799.3	Homo sapiens genomic DNA, chromosome 11q, clone:RP11-806N19, complete sequence	30.2	30.2	100%	33	100%
BX908786.9	Zebrafish DNA sequence from clone CH211-1308 in linkage group 3, complete sequence	30.2	30.2	100%	33	100%
AL807770.17	Mouse DNA sequence from clone RP23-206L14 on chromosome 4, complete sequence	30.2	30.2	100%	33	100%
AL683854.20	Mouse DNA sequence from clone RP23-237K13 on chromosome 4, complete sequence	30.2	30.2	100%	33	100%
AL591514.7	Mouse DNA sequence from clone RP23-266L14 on chromosome 11, complete sequence	30.2	30.2	100%	33	100%

Alignments

>emb|AM468046.2| **D** Vitis vinifera contig VV78X022861.5, whole genome shotgun seq
Length=17913

Score = 30.2 bits (15), Expect = 33
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 GCATTTGTGAAGAGA 15
|||||||||||||||
Sbjct 3572 GCATTTGTGAAGAGA 3558

>gb|AC202214.3| **D** Pea Aphid NOVECTOR VMRC38-20-A9 () complete sequence
Length=102345

Score = 30.2 bits (15), Expect = 33
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 GCATTTGTGAAGAGA 15
|||||||||||||||
Sbjct 40355 GCATTTGTGAAGAGA 40341

>ref|NM_018666.2| **UG** Homo sapiens sarcoma antigen 1 (SAGE1), mRNA
Length=3069

Score = 30.2 bits (15), Expect = 33
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 GCATTTGTGAAGAGA 15
|||||||||||||||
Sbjct 406 GCATTTGTGAAGAGA 420

>gb|CP000660.1| **D** Pyrobaculum arsenaticum DSM 13514, complete genome
Length=2121076

Features in this part of subject sequence:
CRISPR-associated HD domain protein

Score = 30.2 bits (15), Expect = 33
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 1 GCATTTGTGAAGAGA 15
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Sbjct 1027001 GCATTTGTGAAGAGA 1027015

>gb|AC188814.3| **D** Gallus gallus BAC clone CH261-93D11 from chromosome z, comple
sequence
Length=176534

Score = 30.2 bits (15), Expect = 33
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1 GCATTTGTGAAGAGA 15
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Sbjct 161540 GCATTTGTGAAGAGA 161526

NCBI Nucleotide

My NC [Sign In] [Regis]

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Display

 GenBankShow 

Hide:



sequence



all but gene, CDS and mRNA

Range: from to Reverse complemented strand

Features:

 1: NM_018666. Reports Homo sapiens sarc...[gi:145580596]

Links

Comment Features Sequence

LOCUS NM_018666 . 3069 bp mRNA linear PRI 26-JUN-2007
 DEFINITION Homo sapiens sarcoma antigen 1 (SAGE1), mRNA.
 ACCESSION NM_018666
 VERSION NM_018666.2 GI:145580596
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3069)
 AUTHORS Miyahara,Y., Naota,H., Wang,L., Hiasa,A., Goto,M., Watanabe,M.,
 Kitano,S., Okumura,S., Takemitsu,T., Yuta,A., Majima,Y.,
 Lemonnier,F.A., Boon,T. and Shiku,H.
 TITLE Determination of cellularly processed HLA-A2402-restricted novel
 CTL epitopes derived from two cancer germ line genes, MAGE-A4 and
 SAGE
 JOURNAL Clin. Cancer Res. 11 (15), 5581-5589 (2005)
 PUBMED 16061876
 REMARK GeneRIF: MAGE-A4(143-151) and SAGE(715-723) are
 HLA-A2402-restricted CTL epitopes
 REFERENCE 2 (bases 1 to 3069)
 AUTHORS Martelange,V., De Smet,C., De Plaen,E., Lurquin,C. and Boon,T.
 TITLE Identification on a human sarcoma of two new genes with
 tumor-specific expression
 JOURNAL Cancer Res. 60 (14), 3848-3855 (2000)
 PUBMED 10919659
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
 reference sequence was derived from AJ278111.1, AL953870.2,
 CD358947.1 and BF056519.1.
 On Apr 20, 2007 this sequence version replaced gi:8924241.

Summary: This gene belongs to a class of genes that are activated in tumors. These genes are expressed in tumors of different histologic types but not in normal tissues, except for spermatogenic cells and, for some, placenta. The proteins encoded by these genes appear to be strictly tumor specific, and hence may be excellent sources of antigens for cancer immunotherapy. This gene is expressed in sarcomas.

COMPLETENESS: complete on the 3' end.

PRIMARY	REFSEQ_SPAN 1-913 914-914	PRIMARY_IDENTIFIER AJ278111.1 AL953870.2	PRIMARY_SPAN 1-913 11665-11665	COMP
---------	---------------------------------	--	--------------------------------------	------

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1664-1951	CD358947.1	502-789				
1952-2580	AJ278111.1	1952-2580				
2581-3045	BF056519.1	1-465				
3046-3069	AJ278111.1	3046-3069				
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3061 aaaaaaaaaa

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Jun 19 2007 13:56:00